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1: DNA Seq 1993;4(3):177-84

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## Genomic organization of the biotin biosynthetic genes of coryneform bacteria: cloning and sequencing of the bioA-bioD genes from *Brevibacterium flavum*.

Hatakeyama K, Hohama K, Vertes AA, Kobayashi M, Kurusu Y, Yukawa H.

Tsukuba Research Center, Mitsubishi Petrochemical Co. Ltd., Ibaraki, Japan.

Three coryneform bacteria, *Brevibacterium flavum*, *Brevibacterium lactofermentum* and *Corynebacterium glutamicum* have been shown to be able to convert 7-keto-8-aminopelargonic acid to biotin through a biotin synthetic pathway identical to that from *Escherichia coli* (Hatakeyama et al., DNA Sequence, in press, 1993). We report in this paper the cloning and sequencing of the biotin biosynthetic genes encoding the 7,8-diaminopelargonic acid aminotransferase (bioA) and the dethiobiotin synthetase (bioD) of *B. flavum* MJ233, by complementation of *E. coli* bioA and bioD mutants. Both bioA and bioD genes from *B. flavum* were located on a 4.0-kb SalI DNA fragment. Nucleotide sequence analysis of this fragment revealed that these genes consist of a 1272 bp and a 675 bp open reading frame, respectively. The deduced amino acid sequence of the 7,8-diaminopelargonic acid aminotransferase (BioA) is 51.3% and 31.9% identical to that of the *E. coli* and *Bacillus spaeiricus* bioA gene products, respectively. The deduced amino acid sequence of the dethiobiotin synthetase (BioD) is 25.9% and 32.7% identical to that of the *E. coli* and *B. spaeiricus* bioD gene products, respectively. In addition, the genomic organization of the bioA, bioB and bioD genes in *B. flavum* has been shown to be different from that in *E. coli* and *B. spaeiricus*.

PMID: 8161820 [PubMed - indexed for MEDLINE]

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1: Microbiology 1996 Nov;142 ( Pt 11):3295-303

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## Complete sequence and organization of the *Serratia marcescens* biotin operon.

Sakurai N, Akatsuka H, Kawai E, Imai Y, Komatsubara S.

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The nucleotide sequence of the biotin (bio) operon of wild-type *Serratia marcescens* Sr41 was determined. Five ORFs were identified to encode BioA (7,8-diaminopelargonic acid aminotransferase), BioB (biotin synthase), BioF (7-keto-8-aminopelargonic acid synthase), BioC (an enzyme catalysing the synthesis of pimeloyl-CoA) and BioD (dethiobiotin synthase), in this order. The operon was deduced to be transcribed divergently to the left into bioA and to the right into the bioBFCD genes. The promoters and a common predicted operator for both bioA and bioBFCD genes were located between the bioA and bioB genes. The predicted amino acid sequences of these enzymes were similar to the sequences of the corresponding enzymes of *Escherichia coli*. Analysis of expression of the lacZ structural gene fused with the bioA and bioB promoters revealed that the biotin operon was subject to biotin-mediated feedback repression.

PMID: 8969526 [PubMed - indexed for MEDLINE]

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